

## SEQUENCE LISTING

<110> Wang, Yi  
 Mueller, John P.  
 Matis, Louis A.

<120> Chimeric Proteins and uses thereof for the Diagnosis,  
 Prevention, and Treatment of Diabetes

<130> ALX-156 PCT

<140> Not Yet Assigned

<141> 1998-12-18

<150> 60/068,648

<151> 1997-10-22

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:IG1 Fusion  
 Protein

<400> 1

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Tyr	Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr	Arg
						20			25				30		
Arg	Glu	Ala	Glu	Asp	Leu	Asn	Met	Tyr	Ala	Met	Met	Ile	Ala	Arg	Phe
						35		40				45			
Lys	Met	Phe	Pro	Glu	Val	Lys	Glu	Lys	Gly	Met	Ala	Ala	Leu	Pro	Arg
						50		55			60				
Leu	Ile	Ala	Phe	Thr	Ser	Glu	Lys	Cys	Leu	Glu	Leu	Ala	Glu	Tyr	Leu
						65		70		75		80			
Tyr	Asn	Ile	Ile	Lys	Asn	Arg	Glu	Gly	Tyr	Glu	Met	Val	Phe	Asp	Gly
						85		90			95				
Lys	Pro	Gln	His	Thr	Asn	Val	Cys	Phe	Trp	Tyr	Ile	Pro	Pro	Ser	Leu
						100		105			110				
Arg	Thr	Leu	Glu	Asp	Asn	Glu	Glu	Arg	Met	Ser	Arg	Leu	Ser	Lys	Val
						115		120			125				
Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Thr	Met	Val
						130		135		140					
Ser	Tyr	Gln	Pro	Leu	Gly	Asp	Lys	Val	Asn	His	His	His	His	His	His
						145		150		155		160			

<210> 2

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:IG2 Fusion  
 Protein

<400> 2

Met	Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu
1						5				10				15	
Tyr	Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr	Arg
						20		25		30					
Arg	Glu	Ala	Glu	Asp	Leu	Met	Asn	Ile	Leu	Leu	Gln	Tyr	Val	Val	Lys
						35		40			45				
Ser	Phe	Asp	Asn	Met	Tyr	Ala	Met	Met	Ile	Ala	Arg	Phe	Lys	Met	Phe
						50		55		60					

Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala  
 65 70 75 80  
 Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu  
 85 90 95  
 Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met  
 100 105 110  
 Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile  
 115 120 125  
 Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg  
 130 135 140  
 Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly  
 145 150 155 160  
 Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn His His  
 165 170 175  
 His His His His  
 180

&lt;210&gt; 3

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:IG3 Fusion Protein

&lt;400&gt; 3

Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu  
 1 5 10 15  
 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
 20 25 30  
 Arg Glu Ala Glu Asp Leu Met Asn Ile Leu Leu Gln Tyr Val Val Lys  
 35 40 45  
 Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe  
 50 55 60  
 Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala  
 65 70 75 80  
 Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu  
 85 90 95  
 Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met  
 100 105 110  
 Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile  
 115 120 125  
 Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn His His His His His His  
 130 135 140

&lt;210&gt; 4

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:IG4 Fusion Protein

&lt;400&gt; 4

Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu  
 1 5 10 15  
 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
 20 25 30  
 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly  
 35 40 45  
 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln

50	55	60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val		
65	70	75
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp		
85	90	95
Pro Gly Gly Ser Gly Asp Gly Gly Met Asn Ile Leu Leu Gln Tyr		
100	105	110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe		
115	120	125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg		
130	135	140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu		
145	150	155
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile His		
165	170	175
His His His His His		
180		

&lt;210&gt; 5

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: IG5 Fusion Protein

&lt;400&gt; 5

Met Phe Val Asn Gln His Leu Cys	Gly Ser His Leu Val Glu Ala Leu	
1	5	10
Tyr Leu Val Cys Gly Glu Arg Gly	Phe Phe Tyr Thr Pro Lys Thr Arg	
20	25	30
Arg Glu Ala Glu Asp Leu Gln Val	Gly Gln Val Glu Leu Gly Gly	
35	40	45
Pro Gly Ala Gly Ser Leu Gln Pro	Leu Ala Leu Glu Gly Ser Leu Gln	
50	55	60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val		
65	70	75
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp		
85	90	95
Pro Gly Gly Ser Gly Asp Gly Gly Met Asn Ile Leu Leu Gln Tyr		
100	105	110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe		
115	120	125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg		
130	135	140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu		
145	150	155
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly		
165	170	175
Gly Gly Tyr Ile Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu		
180	185	190
Arg Met Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met		
195	200	205
Met Glu Tyr Gly Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys		
210	215	220
Val Asn His His His His His		
225	230	

&lt;210&gt; 6

&lt;211&gt; 393

<212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: IG6 Fusion  
 Protein  
 <400> 6  
 Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu  
 1 5 10 15  
 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
 20 25 30  
 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly  
 35 40 45  
 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln  
 50 55 60  
 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val  
 65 70 75 80  
 Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp  
 85 90 95  
 Pro Gly Gly Ser Gly Asp Gly Gly Met Asn Ile Leu Leu Gln Tyr  
 100 105 110  
 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
 115 120 125  
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg  
 130 135 140  
 Leu Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu  
 145 150 155 160  
 Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly  
 165 170 175  
 Gly Gly Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile Ala Thr Gln  
 180 185 190  
 Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met Val Trp Glu  
 195 200 205  
 Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val Glu Asp Gly  
 210 215 220  
 Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ala Ser Leu Tyr  
 225 230 235 240  
 His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp Cys Glu Asp  
 245 250 255  
 Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr Gln Glu Thr  
 260 265 270  
 Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala Glu Gly Thr  
 275 280 285  
 Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys Val Asn Lys  
 290 295 300  
 Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys Ser Asp Gly  
 305 310 315 320  
 Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val Leu Asn Arg  
 325 330 335  
 Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr Leu Glu His  
 340 345 350  
 Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp Gln Phe Glu  
 355 360 365  
 Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile Leu Lys Ala  
 370 375 380  
 Leu Pro Gln His His His His His His  
 385 390  
 <210> 7

<211> 444  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:IG7 Fusion  
 Protein  
 <400> 7  
 Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu  
 1 5 10 15  
 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
 20 25 30  
 Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly  
 35 40 45  
 Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln  
 50 55 60  
 Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val  
 65 70 75 80  
 Sub A1 > Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp  
 85 90 95  
 Pro Gly Gly Ser Gly Asp Gly Gly Met Asn Ile Leu Leu Gln Tyr  
 100 105 110  
 Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
 115 120 125  
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg  
 130 135 140  
 Leu Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu  
 145 150 155 160  
 Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly  
 165 170 175  
 Gly Gly Tyr Ile Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu  
 180 185 190  
 Arg Met Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met  
 195 200 205  
 Met Glu Tyr Gly Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys  
 210 215 220  
 Val Asn Gly Gly Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile  
 225 230 235 240  
 Ala Thr Gln Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met  
 245 250 255  
 Val Trp Glu Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val  
 260 265 270  
 Glu Asp Gly Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ala  
 275 280 285  
 Ser Leu Tyr His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp  
 290 295 300  
 Cys Glu Asp Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr  
 305 310 315 320  
 Gln Glu Thr Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala  
 325 330 335  
 Glu Gly Thr Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys  
 340 345 350  
 Val Asn Lys Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys  
 355 360 365  
 Ser Asp Gly Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val  
 370 375 380  
 Leu Asn Arg Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr  
 385 390 395 400

Leu Glu His Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp  
                   405                        410                        415  
 Gln Phe Glu Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile  
                   420                        425                        430  
 Leu Lys Ala Leu Pro Gln His His His His His His His His His  
                   435                        440

<210> 8  
 <211> 173  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:IG4NHB  
        hypothetical fusion protein  
 <400> 8

Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu  
   1                  5                          10                        15  
 Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg  
   20                  25                        30

Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly  
   35                  40                        45

Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln  
   50                  55                        60

Lys Arg Gly Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp  
   65                  70                        75                        80

Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe Pro Glu Val  
   85                  90                        95

Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala Phe Thr Ser  
   100                 105                        110

Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu Ala Glu Tyr  
   115                 120                        125

Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp  
   130                 135                        140

Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser  
   145                 150                        155                        160

Leu Arg Thr Leu Glu Asp Asn His His His His His His His His  
   165                 170

<210> 9  
 <211> 3  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:Helix breaker  
 <400> 9

Pro Pro Pro  
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<210> 10  
 <211> 3  
 <212> PRT  
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 <220>  
 <223> Description of Artificial Sequence:Helix breaker  
 <400> 10

Gly Gly Gly  
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<210> 11  
 <211> 139  
 <212> DNA

<213> Artificial Sequence  
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 <223> Description of Artificial Sequence:prIG1 primer  
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 tgcggtaaac gcccgtttt ctacaccccg aaaacccgtc gtgaagcgga agatctgaac 120  
 atgtatgcca tgatgatcg 139  
 <210> 12  
 <211> 143  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG2 primer  
 <400> 12  
 ggtttttaat gatgttgtac agatattccg ccagttccag acattttca gaggtaaagg 60  
 caatcagacg cggttagcgcg gccatacctt tttcttaac ttccggaaac attttaaagc 120  
 gcgcgatcat catggcatac atg 143  
 <210> 13  
 <211> 138  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG3 primer  
 <400> 13  
 gtacaacatc attaaaaacc gcgaaggcta tgaaatggtt ttcgatggta aaccgcagca 60  
 taccaacgtt tgcttttgtt acatcccggc gagcctgcgt accctggaaat aacgaaga 120  
 acgcgtatgac cgtctgtc 138  
 <210> 14  
 <211> 132  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG4 primer  
 <400> 14  
 ggatccttaa tggtgatggt gatggtggtt aacttatca cccagccgct ggttagctaac 60  
 catggtggtt ccatattcca tcatgcgcgc ttataataacc gggcaactt tagacagacg 120  
 gctcatgcgt tc 132  
 <210> 15  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG5 primer  
 <400> 15  
 catatgttcg ttaaccag 18  
 <210> 16  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG6 primer  
 <400> 16  
 ggatccttaa tggtgatg 18  
 <210> 17  
 <211> 492  
 <212> DNA  
 <213> Artificial Sequence

<220> Description of Artificial Sequence:IG1 Fusion  
Protein coding sequence

<210> 17

catatgttcg ttaaccagca tctgtgtggc tctcacctgg ttgaagccct gatatctggtt 60  
tgcggtaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgaac 120  
atgttatgcca tgatgatcgc gcgcttaaa atgttcccg aagttaaaga aaaaggatg 180  
gccgcgtgc cgctgtat tgccttacc tctgaaaaat gtctgaact ggcgaaatat 240  
ctgtacaaca tcattaaaaa ccgcgaaggc tatgaaatgg tttcgatgg taaaccgcag 300  
cataccaacg tttgttttg gtacatccc cgcgcctgc gtaccctgga agataacgaa 360  
gaacgcatga ggcgtctgtc taaagttgcc ccggttatta aagcgcgcatt gatgaaatat 420  
ggcaccacca tggtagcta ccagccgctg ggtgataaag ttaaccacca tcaccatcac 480  
cattaaggat cc 492

<210> 18

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prIG7 primer

<400> 18

agatctgatg aacattctgc tgcagtatgt tgttaaaagc ttgcataaca tgtatgccat 60  
gatg 64

<210> 19

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prIG8 primer

<400> 19

tgtacagata ttccgcccagt tccagacatt ttttcagaga aaaatggcta tggtagagg 60  
taaaggcaat cagacgcg 78

<210> 20

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prIG12 primer

<400> 20

tgtacagata ttccgcccagt tccagac 27

<210> 21

<211> 552

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:IG2 Fusion  
Protein coding sequence

<400> 21

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tgcggtaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgatg 120  
aacattctgc tgcagtatgt tgttaaaagc ttgcataaca tgtatgccat gatgatcg 180  
cgctttaaaa tggcccgaa agttaaagaa aaaggatgg ccgcgcgtgc ggcgtctgatt 240  
gccttaccc tctgaacatag ccattttct ctgaaaaat gtctgaact ggcgaaatat 300  
ctgtacaaca tcattaaaaa ccgcgaaggc tatgaaatgg tttcgatgg taaaccgcag 360  
cataccaacg tttgttttg gtacatccc cgcgcctgc gtaccctgga agataacgaa 420  
gaacgcatga ggcgtctgtc taaagttgcc ccggttatta aagcgcgcatt gatgaaatat 480  
ggcaccacca tggtagcta ccagccgctg ggtgataaag ttaaccacca tcaccatcac 540  
cattaaggat cc 552

<210> 22  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG13 primer  
 <400> 22  
 ggatccttaa atgggtatgg tggatgggt tatcttccag ggtacg 46  
 <210> 23  
 <211> 444  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:IG3 Fusion  
 Protein coding sequence  
 <400> 23  
 catatgttcg ttaaccagca tctgtgtggc tctcacctgg ttgaaggccct gtatctgggt 60  
 tgcggtaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgatg 120  
 aacattctgc tgcatgtatgt tgttaaaagc ttgcataaca tgtatgccat gatgatcg 180  
 cgctttaaaa tggcccgga agttaaagaa aaaggatgg ccgcgcgtgcc gcgtctgatt 240  
 gccttacct ctgaacatag ccattttct ctgaaaaat gtctggact ggccgaatat 300  
 ctgtacaaca tcattaaaaa ccgcgaaggc tatgaaatgg tttcgatgg taaaccgcag 360  
 cataccaacg tttgctttt gtacatccc ccgagcctgc gtaccctgga agataaccac 420  
 catcaccatc accattaagg atcc 444  
 <210> 24  
 <211> 555  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:IG4 Fusion  
 Protein coding sequence  
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 tgcggtaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgc 120  
 gtggggcagg tggagctggg cggggccct ggtgcaggca gcctgcagcc ctggccctg 180  
 gaggggtccc tgcagaagcg tggactaac atgttacccat atgaaatgc tcaggatatt 240  
 gtgctttgg aatatgtcac actaaagaaa atgagagaaa tcattggctg gccagggggc 300  
 tctggcgatg gaggcggtat gaacattctg ctgcagtatg ttgttaaaag ctgcataac 360  
 atgtatgcca tggatgtatgc ggccttaaa atgttcccg aagttaaaga aaaaggatg 420  
 ggcgcgtgc cgcgtctggg aggccgtatt gccttacct ctgaacatag ccattttct 480  
 ctgaaaaaag gagctgcagc ctttagggatt ggaacagaca gcgtgattca ccatcaccat 540  
 caccattaag gatcc 555  
 <210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence:prIG14 primer  
 <400> 25  
 catatgttcg ttaaccagca tctg 24  
 <210> 26  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG15 primer  
 <400> 26

gctgcctgca ccagggcccc cgcccagctc cacctgcccc acctgcagat cttccgcttc 60  
 acgacgggt 69

<210> 27  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG16 primer  
 <400> 27  
 agtgcacgc ttctgcaggg acccctccag ggccaagggc tgcaggctgc ctgcaccagg 60  
 gcccc 66  
 <210> 28  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG17 primer  
 <400> 28  
 ttccaaaagc acaaatactg gagcaatttc ataggtgaac atgttagtgc cacgcttctg 60  
 cagggaccc 69  
 <210> 29  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence A  
 <220>  
 <223> Description of Artificial Sequence:prIG18 primer  
 <400> 29  
 ccctggccag ccaatgattt ctctcatttt ctttagtgtg acatattcca aaagcacaaa 60  
 tactggagc 69  
 <210> 30  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG19 primer  
 <400> 30  
 agagaaaatca ttggctggcc agggggctct ggcgatggag gcggtatgaa cattctgctg 60  
 cagtatgtt 69  
 <210> 31  
 <211> 68  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG20 primer  
 <400> 31  
 cagagaaaaa tggctatgtt cagaggtaaa ggcaataccg cctccagac gcggcagcgc 60  
 ggccatac 68  
 <210> 32  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:prIG21 primer  
 <400> 32  
 aatcacgctg tctgttccaa tccctaaggc tgcagctcct ttttcagag aaaaatggct 60

69

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atgttcaga
<210> 33
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:prIG22 primer
<400> 33
ttagggattg gaacagacag cgtgatttga ggccgttaca tcccgccgag cctgcgtacc 60
<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:prIG23 primer
<400> 34
ggatccttaa tggtgatggt gatg

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24

*Sub A1*

*A*

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<210> 35
<211> 708
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:IG5 Fusion
    Protein coding sequence
<400> 35
catatgttcg ttaaccagca tctgtgtggc tctcacctgg ttgaaggccct gtatctggtt 60
tgccgtgaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgcag 120
gtggggcagg tggagctggg cggggggccct ggtgcaggca gcctgcagcc cttggccctg 180
gaggggtccc tgcagaagcg tggactaac atgttccacct atgaaattgc tccagtattt 240
gtgcttttgg aatatgtcac actaaagaaa atgagagaaa tcattggctg gccagggggc 300
tctggcgatg gaggcggtat gaacattctg ctgcagtatg ttgttaaaag cttcgataaac 360
atgtatgcc a tcatgtatcg ggcgtttaaa atgttcccg aagttaaaga aaaaggatag 420
gccgcgtgc cgctgttggg aggccgtatt gccttacact ctgaacatag ccattttct 480
ctgaaaaaaag gagctgcagc cttaggatt ggaacagaca gcgtgattgg aggccgttac 540
attcctccaa gcttgcgtac tctggaaagac aatgaagaac gcatgagccg tctgtctaaa 600
gttgcggccgg ttattnaagc ggcgtatgtt gaaatggca ccaccatgg tagctaccag 660
ccgctgggtt ataaagttaa ccaccatcac catcaccatt aaggatcc

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708

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<210> 36
<211> 1191
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:IG6 Fusion
    Protein coding sequence
<400> 36
catatgttcg ttaaccagca tctgtgtggc tctcacctgg ttgaaggccct gtatctggtt 60
tgccgtgaac gcggctttt ctacaccccg aaaacccgtc gtgaagcgga agatctgcag 120
gtggggcagg tggagctggg cggggggccct ggtgcaggca gcctgcagcc cttggccctg 180
gaggggtccc tgcagaagcg tggactaac atgttccacct atgaaattgc tccagtattt 240
gtgcttttgg aatatgtcac actaaagaaa atgagagaaa tcattggctg gccagggggc 300
tctggcgatg gaggcggtat gaacattctg ctgcagtatg ttgttaaaag cttcgataaac 360
atgtatgcc a tcatgtatcg ggcgtttaaa atgttcccg aagttaaaga aaaaggatag 420
gccgcgtgc cgctgttggg aggccgtatt gccttacact ctgaacatag ccattttct 480
ctgaaaaaaag gagctgcagc cttaggatt ggaacagaca gcgtgattgg aggccgttac 540
gagcatgacc ctcggatgcc agcctacata ggcacgcagg gcccgcgtgc ccataccatc 600
gcagacttct ggcagatggt gtgggagagc ggctgcaccg tcatcgatcat gctgaccccg 660
ctgggtggagg atgggtgtcaa gcagtgtgac cgctactggc cagatgaggg tgcctccctc 720

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taccacgtat atgaggtgaa cctgggtcg gaggcacatct ggtgcgagga ctttctgg 780  
 cggagcttct acctgaagaa cgtgcagacc caggagacgc gcacgcac gcagttccac 840  
 ttccctcagct ggccggcaga gggcacaccg gcctccacgc ggccccctgct ggacttccgc 900  
 aggaagggtga acaagtgcata ccggggccgc tcctgccccca tcatacgatcgat 960  
 ggtgcggggga ggaccggcac ctacatcctc atcgacatgg tcctgaaccg catggcaaaa 1020  
 ggagtgaagg agattgacat cgctgccacc ctggagcatg tccgtgacca gcggcctggc 1080  
 cttgtccgct ctaaggacca gttgaattt gccctgacag ccgtggcgga ggaagtgaat 1140  
 gccatcctca aggccctgcc ccagcaccat caccatcacc attaaggatc c 1191

&lt;210&gt; 37

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: IG7 Fusion  
Protein coding sequence

&lt;400&gt; 37

catatgttcg ttaaccagca tctgtgtggc ttcacacctgg ttgaaggccc gtatctgg 60  
 tgcgggtgaac gcggctttt ctacacccccc aaaacccgtc gtgaaggcgga agatctgcag 120  
 gtggggcagg tggagctggg cggggggccct ggtgcaggca gcctgcagcc cttggccctg 180  
 gaggggtccc tgcagaagcg tggactaac atgttcaccc atgaaattgc tccagtattt 240  
 gtgctttgg aatatgtcac actaaagaaaa atgagagaaaa tcattggctg gccagggggc 300  
 tctggcgatg gaggcggtat gaacattctg ctgcagtgatg ttgttaaaag cttcgataac 360  
 atgtatgcca tgatgatcgc gcgccttaaa atgttcccg aagttaaaga aaaaggatag 420  
 gccgcgcgtgc cgcgtctggg aggccgtatt gccttaccc ctgaacatag ccattttct 480  
 ctgaaaaaaag gagctgcagc cttagggatt ggaacagaca ggtgtattgg aggccgttac 540  
 attcctccaa gcttgcgtac tcttggaaagac aatgaagaac gcatgagccg tctgtctaaa 600  
 gttgccccgg ttattaaagc gcgcgtatgc gaatatggca ccaccatgg tagtaccag 660  
 ccgcgtgggtg ataaagttaa cggaggccgt attgagcatg accctcgat gccagcctac 720  
 atagccacgc agggcccgt gtccatacc atcgacact tctggcagat ggtgtgggag 780  
 agcggctgca ccgtcatcgt catgctgacc ccgcgtggg aggatgtgt caagcagtgt 840  
 gaccgcgtact ggccagatga ggggcctcc ctctaccacg tataatggat gaaacctgg 900  
 tcggagcaca tctggtgcgaa ggacttctg gtgcggagct tctacctgaa gaaatgtcag 960  
 acccaggaga cgcgcacgt cacgcgttcc cacttcctca gctggccggc agagggcaca 1020  
 ccggcctcca cgcggccct gctggacttc cgcaggaaagg tgaacaagtgc ctaccggggc 1080  
 cgctcctgcc ccatcatcgt gcactgcgt gatggcgg ggaggaccgg cacctacatc 1140  
 ctcatcgaca tggcctgaa ccgcgtggca aaaggagatgaa aggagattga catcgctgcc 1200  
 accctggagc atgtccgtga ccagccgtcc ggccttgc gctctaagga ccagtttggaa 1260  
 tttggccctga cagccgtggc ggaggaagtg aatgcacatcc tcaaggccct gccccagcac 1320  
 catcaccatc accattaagg atcc 1344

Sub A1